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Multi-Omics Approaches for the Bioremediation of Heavy Metal Contamination

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Abstract

Heavy metals (HMs) are non-biodegradable and can accumulate in soil and aquatic environments for longer periods. These HMs also induce serious effects on humans by eating the contaminated foods grown in such soil/water. Bioremediation is gaining attention in recent years as an environmentally friendly and cost-effective method for removal of heavy metals. Comprehensive investigation of microbial communities and their metabolism can be easily facilitated using Multi-omics technologies which has enabled the development of many other advanced remediation strategies. Genomics deals with identification of specific genes involved in HMs resistance, transformation, and detoxification. Metagenomics provides analysis of microbial communities present in contaminated environments culture-independently and their genes involved in detoxification within HMs contaminated sites. Transcriptomics enables and identifies patterns of gene expression under HM exposure. Proteomics focuses on the proteins expressed during bioremediation processes. Metabolomics, fluxomics and system biology are other omics approaches discussed in this review. It also highlights the importance of integration of AI and Machine learning to predict optimized bioremediation strategies and outline the future prospects for efficient and safe HM bioremediation approaches.

Keywords: Heavy metals, Bioremediation, Multi-omics, Metagenomics, Transcriptomics, Proteomics

Introduction

Increasing industrial and anthropogenic activities along with rapidly increasing population is resulting in heavy metal pollution. Heavy metals are non-biodegradable and can accumulate in soil and aquatic environments for longer periods (Islam et al., 2024). Their persistence leads to less agricultural productivity, ecological imbalance, and several neurological health issues in humans. Moreover, due to their accumulation, they become carcinogenic and can cause organ failure (Asyakina et al., 2021;).

Global agricultural communities have serious concern over threat of heavy metals (HMs) contamination of agricultural soils. These HMs are highly toxic and they can remain in the soils over a long time period. Majorly applied organic and inorganic fertilizers contains HMs such as cadmium (Cd), copper (Cu), lead (Pb), and zinc (Zn) while excreted industrial HMs are arsenic (As) and mercury (Hg). They both enter into agricultural soils and accumulate overthere. (Guan et al., 2022). and these HMs also induce serious effects on humans by eating the contaminated foods

Bioremediation is gaining attention in recent years as an environmentally friendly and cost-effective method for removal of heavy metals. Microorganisms and plants transform heavy metal into less toxic substances and thus several studies have employed them for heavy metal treatment from wastewater or other polluted sources. Phytoremediation and microbial remediation have emerged as sustainable alternatives for mitigating heavy metal contamination. Understanding the microbial metabolic processes, interaction and microbial networks during heavy metal removal and remediation is still challenging due to its complexity which needs usage of emerging technologies. Thorough investigation of microbial communities and their metabolism can be easily facilitated using multi-omics technologies which has enabled the development of many other advanced remediation strategies (Deo et al 2024).

Concept of Multi-Omics in HMs Bioremediation

Multi-omics is the integration of multiple biological datasets to understand a complete picture of complex biological systems. It comprises various omics platforms (genomics, proteomics, transcriptomics, metabolomics, and other) to give insight into a microbial functions and interactions.

1. Genomics and Metagenomics

Genomics deals with identification of specific genes involved in HMs resistance, transformation, and detoxification. Metagenomics provides analysis of microbial communities present in contaminated environments culture-independently and their genes involved in detoxification within HMs contaminated sites. This allows scientists to design bioremediation strategies which are aligned and mapped with HMs-resistant bacteria such as *Pseudomonas* or *Bacillus* species. [Li et al 2023]. Many genomics and metagenomics studies thus help in discovery of HM resistant microorganisms, characterization of structure of microbial community, identification of HM resistance genes and functional annotation of HM biodegradation pathways. Metagenomic studies have revealed diverse microbial populations capable of surviving and functioning under extreme HM stress conditions. (Chettri et al, 2024)

2. Transcriptomics

Transcriptomics enables and identifies patterns of gene expression under HM exposure. RNA sequencing facilitates identifying genes activated during HM detoxification. Many Important findings include altered regulation (upregulation mostly) of metal transporters, activation of genes pertaining oxidative stress response, overexpression of metal-chelating proteins and regulation of efflux pump systems (Zhang et al., 2026). Overall, transcriptomic study helps in revealing microbial responses generated during exposure to environmental HM stress and enables designing of optimized bioremediation strategies optimized to particular HM stress.

3. Proteomics

Proteomics focuses on the proteins expressed during bioremediation processes. As proteins directly catalyze biochemical reactions, proteomic studies provide direct representation of detoxification mechanisms of HMs. Transcriptomic findings are often complemented with Proteomic data, provide validation of functional pathways. Proteomic data directly deals with identification of HM-binding proteins and stress-response enzymes. These both assist in finding microbial adaptation mechanisms (Chakdar et al., 2022). Techniques like mass spectrometry highlights the mechanism of altered protein expression under stress, which eventually leads to innovation of novel biomarkers for HM contaminated environment (Ilyas et al., 2024)

4. Metabolomics

Metabolomics investigates small molecules and metabolic intermediates of cellular processes. Metabolomics provides a direct insight of various cellular states during bioremediation by detecting metabolic alterations under HM stress and Identification of detoxification metabolites (Sharma et al., 2023). This approach has been extended to understand microbial metabolic networks and monitoring of bioremediation efficacy (Smith et al., 2024)

5. Fluxomics and Systems Biology

Fluxomics offers detailed and comprehensive analysis of metabolic fluxes through biochemical pathways, thus gives quantitative assessment of microbial metabolism. Integration of fluxomics with systems biology can provide optimized models for bioremediation performance.

Differing with metabolomics, fluxomics monitors metabolic pathway activity constitutively which determine HM involved in altering biochemical processes quantitatively. [Emwas et al, 2022]

Multi-Omics Integration for Heavy Metal Bioremediation

Integration of omics datasets discussed above evaluates holistic understanding of ecosystem of microbes by combining all omics approaches altogether. Recent studies demonstrate that multi-omics integration significantly improves the accuracy of biochemical pathway reconstruction and functional predictions in HM contaminated environments (Raza et al., 2022, 2024).

Artificial Intelligence and Multi-Omics Integration

To improve HM bioremediation and application of Omics approaches into it, artificial intelligence (AI) and machine learning (ML) are nowadays integrated with datasets of multiomics which give transformative opportunities to overcome limitations linked with HM bioremediation. In one of the recent study, integration of AI-driven models with multiomics data is utilized to predict the plant-microbe interactions thus utilized for optimizing phytoremediation strategies. AI enables the selection of plant growth-promoting bacteria (PGPB), and modeling of dynamic study of metal transporter eventually leads to enhanced crop tolerance and HM accumulation. By mining large-scale omics datasets, AI can mine enormous omics data at a time and thereby elucidate critical pathways for HM detoxification and guide for prospective engineering of plants and microbes. AI, ML, and multi-omics technologies convergence has transformed the approach to solving the challenge of HMs pollution in soils. (Gul et al., 2025) The integrated framework prepares for next-generation environmental remediation systems.

Future Perspectives

Omics technologies have fundamentally transformed our understanding of how plant and microorganisms resist and survive with HM toxicity. Mapping datasets obtained from multi-omics (genetic, transcriptomic, proteomic, and metabolic) technologies, researchers are now capable of designing efficient, novice and tailored bioremediation strategies.

However, computational and bioinformatics challenges are always there with the massive multi-omics data, future research must focus on overcoming those computational challenges. Moreover, open field trials must be an

important step to critically examine bioremediation followed with laboratory-based omics findings. The spatial omics holds notable potential for further revelation of cell and tissue specific mechanisms of HM detoxification.

Conclusion

This review revealed the bioremediation as a better substitute for the removal of HM from contaminated sources compared to the conventional methods which are less efficient and expensive. Phytoremediation and microbial bioremediation remove the metals from the environment in a harmless manner. Multi-omics technologies have transformed environmental bioremediation research by facilitating in-depth understanding of microbial communities and their functional pathways. Integration of all omics approaches provides unprecedented insights into HM detoxification mechanisms. The incorporation of AI and machine learning further provide strength to the multi-omics-catalyzed bioremediation strategies. Most recent advancements in these technologies will further accelerate the development of sustainable, and environmentally friendly solutions efficiently for mitigating HM contamination.

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Conflicts of interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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